

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/562,469  
Source: JEWOP  
Date Processed by STIC: 07/07/2006

**ENTERED**



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/562,469**

**DATE: 07/07/2006**  
**TIME: 14:20:05**

Input Set.: E:\405uspc.app.txt  
Output Set: N:\CRF4\07072006\J562469.raw

3 <110> APPLICANT: Masato MIYAKE  
4 Tomohiro YOSHIKAWA  
5 Jun MIYAKE  
7 <120> TITLE OF INVENTION: Digital cell  
9 <130> FILE REFERENCE: 690121.405USPC  
11 <140> CURRENT APPLICATION NUMBER: US 10/562,469  
C--> 12 <141> CURRENT FILING DATE: 2005-12-22  
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/009404  
15 <151> PRIOR FILING DATE: 2004-06-25  
17 <150> PRIOR APPLICATION NUMBER: JP 2003-289469  
18 <151> PRIOR FILING DATE: 2003-08-07  
20 <150> PRIOR APPLICATION NUMBER: JP 2003-181915  
21 <151> PRIOR FILING DATE: 2003-06-25  
23 <160> NUMBER OF SEQ ID NOS: 50  
25 <170> SOFTWARE: PatentIn version 3.1  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 1929  
29 <212> TYPE: DNA  
30 <213> ORGANISM: Homo sapiens  
32 <220> FEATURE:  
33 <221> NAME/KEY: CDS  
34 <222> LOCATION: (1)..(1929)  
35 <223> OTHER INFORMATION: fibronectin 1  
38 <400> SEQUENCE: 1  
39 atg ctt agg ggt ccg ggg ccc ggg ctg ctg ctg gcc gtc cag tgc 48  
40 Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Ala Val Gln Cys  
41 1 5 10 15  
43 ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag 96  
44 Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
45 20 25 30  
47 gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc 144  
48 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
49 35 40 45  
51 aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag 192  
52 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
53 50 55 60  
55 tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat gga 240  
56 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
57 65 70 75 80  
59 gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act 288  
60 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
61 85 90 95  
63 tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act tat 336

(Pg 6)

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64 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr		
65 100 105 110		
67 gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg gct	384	
68 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala		
69 115 120 125		
71 ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa ggg	432	
72 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly		
73 130 135 140		
75 ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag act	480	
76 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr		
77 145 150 155 160		
79 ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga gaa	528	
80 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu		
81 165 170 175		
83 tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct ggg	576	
84 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly		
85 180 185 190		
87 act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc tgg	624	
88 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp		
89 195 200 205		
91 atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc act	672	
92 Met Met Val Asp Cys Thr Cys Leu Gly Glu Ser Gly Arg Ile Thr		
93 210 215 220		
95 tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc tat	720	
96 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr		
97 225 230 235 240		
99 aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg ctc	768	
100 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu		
101 245 250 255		
103 cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag agg	816	
104 Gln Cys Ile Cys Thr Gly Asn Gly Arg Glu Trp Lys Cys Glu Arg		
105 260 265 270		
107 cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc gat	864	
108 His Thr Ser Val Gln Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp		
109 275 280 285		
111 gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct ccc	912	
112 Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro		
113 290 295 300		
115 tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg atg	960	
116 Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met		
117 305 310 315 320		
119 cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc ctg	1008	
120 Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu		
121 325 330 335		
123 ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac ggt	1056	
124 Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly		
125 340 345 350		
127 ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat ggc	1104	
128 Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly		

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Input Set : E:\405uspc.app.txt  
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129	355	360	365	
131	agg acg gac agc aca act tcg aat tat gag cag gac cag aaa tac tct			1152
132	Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser			
133	370	375	380	
135	ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc			1200
136	Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser			
137	385	390	395	400
139	aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac			1248
140	Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr			
141	405	410	415	
143	act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg			1296
144	Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly			
145	420	425	430	
147	acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg			1344
148	Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met			
149	435	440	445	
151	gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc			1392
152	Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg			
153	450	455	460	
155	att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg			1440
156	Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg			
157	465	470	475	480
159	tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac			1488
160	Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr			
161	485	490	495	
163	tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg			1536
164	Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val			
165	500	505	510	
167	aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt			1584
168	Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys			
169	515	520	525	
171	aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac			1632
172	Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp			
173	530	535	540	
175	caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca			1680
176	Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser			
177	545	550	555	560
179	tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc			1728
180	Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly			
181	565	570	575	
183	cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc			1776
184	Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser			
185	580	585	590	
187	tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc			1824
188	Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro			
189	595	600	605	
191	aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc			1872
192	Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser			
193	610	615	620	

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Input Set : E:\405uspc.app.txt

Output Set: N:\CRF4\07072006\J562469.raw

195 aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt      1920  
 196 Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu  
 197 625                        630                        635                        640  
 199 gga tac tga  
 200 Gly Tyr  
 204 <210> SEQ ID NO: 2  
 205 <211> LENGTH: 642  
 206 <212> TYPE: PRT  
 207 <213> ORGANISM: Homo sapiens  
 209 <400> SEQUENCE: 2  
 211 Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Ala Val Gln Cys      15  
 212 1                        5                            10                        15  
 215 Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
 216                        20                            25                        30  
 219 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
 220                        35                            40                        45  
 223 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
 224                        50                            55                        60  
 227 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
 228 65                        70                            75                        80  
 231 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
 232                        85                            90                        95  
 235 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
 236                        100                            105                        110  
 239 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
 240                        115                            120                        125  
 243 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
 244                        130                            135                        140  
 247 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
 248 145                        150                            155                        160  
 252 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
 253                        165                            170                        175  
 256 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
 257                        180                            185                        190  
 260 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
 261                        195                            200                        205  
 264 Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
 265                        210                            215                        220  
 268 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
 269 225                        230                            235                        240  
 272 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
 273                        245                            250                        255  
 276 Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg  
 277                        260                            265                        270  
 280 His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp  
 281                        275                            280                        285  
 284 Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro  
 285                        290                            295                        300  
 288 Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met

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289	305	310	315	320
292	Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu			
293	325	330	335	
296	Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly			
297	340	345	350	
300	Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly			
301	355	360	365	
304	Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser			
305	370	375	380	
308	Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser			
309	385	390	395	400
312	Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr			
313	405	410	415	
316	Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly			
317	420	425	430	
320	Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met			
321	435	440	445	
324	Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg			
325	450	455	460	
328	Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg			
329	465	470	475	480
332	Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr			
333	485	490	495	
336	Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val			
337	500	505	510	
340	Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys			
341	515	520	525	
344	Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp			
345	530	535	540	
348	Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser			
349	545	550	555	560
352	Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly			
353	565	570	575	
356	Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser			
357	580	585	590	
360	Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro			
361	595	600	605	
364	Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser			
365	610	615	620	
368	Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu			
369	625	630	635	640
372	Gly Tyr			
376	<210> SEQ ID NO: 3			
377	<211> LENGTH: 1437			
378	<212> TYPE: DNA			
379	<213> ORGANISM: Mus musculus			
381	<220> FEATURE:			
382	<221> NAME/KEY: CDS			
383	<222> LOCATION: (1)..(1437)			

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 07/07/2006  
PATENT APPLICATION: US/10/562,469               TIME: 14:20:06

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; N Pos. 99  
Seq#:31; N Pos. 3  
Seq#:33; N Pos. 15  
Seq#:35; N Pos. 108  
Seq#:37; N Pos. 940,1083  
Seq#:37; Xaa Pos. 286  
Seq#:38; Xaa Pos. 286

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:12; Line(s) 4237

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:12,47,48

**VERIFICATION SUMMARY**

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:4240 M:112 C: (48) String data converted to lower case,  
L:4661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:60  
L:5958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0  
L:6177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0  
L:6380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:60  
L:6672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:929  
L:6673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:977  
L:6684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:1080  
L:6767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:272